

Serial Number: 09/405,735

ENTERED

Changed a file from non-ASCII to ASCII

Changed the margins in cases where the sequence text was "wrapped" down to the next line.

Edited a format error in the Current Application Data section, specifically:

Edited the Current Application Data section with the actual current number. The number inputted by the applicant was the prior application data; or other _____

Added the mandatory heading and subheadings for "Current Application Data".

Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

Changed the spelling of a mandatory field (the headings or subheadings), specifically:

Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: 1

Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

Inserted colons after headings/subheadings. Headings edited included: **RECEIVED**

Deleted extra, invalid, headings used by an applicant, specifically:

MAY 30 2000

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Deleted: non-ASCII "garbage" at the beginning/end of files; secretary initials/filename at end of file; page numbers throughout text; other invalid text, such as _____

Inserted mandatory headings, specifically:

Corrected an obvious error in the response, specifically:

Edited identifiers where upper case is used but lower case is required, or vice versa.

Corrected an error in the Number of Sequences field, specifically:

A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

Other: Sign / e - 2 - aligned one w and two

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/405,735

DATE: 05/15/2000
TIME: 13:25:57

Input Set : A:\Pto.amc
Output Set: N:\CRF3\05152000\I405735.raw

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4 <110> APPLICANT: Pier, Gerald B.
6 <120> TITLE OF INVENTION: Methods and Products for Treating
7     Pseudomonas Infection
9 <130> FILE REFERENCE: B0801/7155 (HCL)
11 <140> CURRENT APPLICATION NUMBER: 09/405,735
12 <141> CURRENT FILING DATE: 1999-09-24
14 <150> PRIOR APPLICATION NUMBER: US 08/681,838
15 <151> PRIOR FILING DATE: 1996-07-29
17 <160> NUMBER OF SEQ ID NOS: 4
19 <170> SOFTWARE: FastSEQ for Windows Version 3.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 6129
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo Sapiens
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (133)...(4575)
30 <400> SEQUENCE: 1
31 aattggaagc aaatgacatc acagcaggtc agagaaaaag gttttagcgcc cggcacc 60
32 gagtagtagg tctttggcat taggagcttgc agccccagacg gccttagcag ggacccc 120
33 gcccggaga cc atg cag agg tcg cct ctg gaa aag gcc agc gtt gtc tcc 171
34             Met Gln Arg Ser Pro Leu Glu Lys Ala Ser Val Val Ser
35             1           5           10
36             15          20          25
37 aaa ctt ttt ttc agc tgg acc aga cca att ttg agg aaa gga tac aga 219
38 Lys Leu Phe Phe Ser Trp Thr Arg Pro Ile Leu Arg Lys Gly Tyr Arg
39             15          20          25
40 cag cgc ctg gaa ttg tca gac ata tac caa atc cct tct gtt gat tct 267
42 Gln Arg Leu Glu Leu Ser Asp Ile Tyr Gln Ile Pro Ser Val Asp Ser
43             30          35          40          45
44 gct gac aat cta tct gaa aaa ttg gaa aga gaa tgg gat aga gag ctg 315
46 Ala Asp Asn Leu Ser Glu Lys Leu Glu Arg Glu Trp Asp Arg Glu Leu
47             50          55          60
48 gct tca aag aaa aat cct aaa ctc att aat gcc ctt cggtt gat ttt 363
50 Ala Ser Lys Lys Asn Pro Lys Leu Ile Asn Ala Leu Arg Arg Cys Phe
51             65          70          75
52 ttc tgg aga ttt atg ttc tat gga atc ttt tta tat tta ggg gaa gtc 411
54 Phe Trp Arg Phe Met Phe Tyr Gly Ile Phe Leu Tyr Leu Gly Glu Val
55             80          85          90
56 acc aaa gca gta cag cct ctc tta ctg gga aga atc ata gct tcc tat 459
58 Thr Lys Ala Val Gln Pro Leu Leu Gly Arg Ile Ile Ala Ser Tyr
59             95          100         105
60 gac ccg gat aac aag gag gaa cgc tct atc gcg att tat cta ggc ata 507
62 Asp Pro Asp Asn Lys Glu Glu Arg Ser Ile Ala Ile Tyr Leu Gly Ile
63             110         115         120         125
64 ggc tta tgc ctt ctc ttt att gtg agg aca ctg ctc cta cac cca gcc 555
66 Gly Leu Cys Leu Leu Phe Ile Val Arg Thr Leu Leu His Pro Ala
67             130         135         140

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70	Ile Phe Gly Leu His His Ile Gly Met Gln Met Arg Ile Ala Met Phe	
71	145 150 155	
73	agt ttg att tat aag aag act tta aag ctg tca agc cgt gtt cta gat	651
74	Ser Leu Ile Tyr Lys Lys Thr Leu Lys Leu Ser Ser Arg Val Leu Asp	
75	160 165 170	
77	aaa ata agt att gga caa ctt gtt agt ctc ctt tcc aac aac ctg aac	699
78	Lys Ile Ser Ile Gly Gln Leu Val Ser Leu Leu Ser Asn Asn Leu Asn	
79	175 180 185	
81	aaa ttt gat gaa gga ctt gca ttg gca cat ttc gtg tgg atc gct cct	747
82	Lys Phe Asp Glu Gly Leu Ala Leu Ala His Phe Val Trp Ile Ala Pro	
83	190 195 200 205	
85	ttg caa gtg gca ctc ctc atg ggg cta atc tgg gag ttg tta cag gcg	795
86	Leu Gln Val Ala Leu Leu Met Gly Leu Ile Trp Glu Leu Leu Gln Ala	
87	210 215 220	
89	tct gcc ttc tgt gga ctt ggt ttc ctg ata gtc ctt gcc ctt ttt cag	843
90	Ser Ala Phe Cys Gly Leu Gly Phe Leu Ile Val Leu Ala Leu Phe Gln	
91	225 230 235	
93	gct ggg cta ggg aga atg atg aag tac aga gat cag aga gct ggg	891
94	Ala Gly Leu Gly Arg Met Met Lys Tyr Arg Asp Gln Arg Ala Gly	
95	240 245 250	
97	aag atc agt gaa aga ctt gtg att acc tca gaa atg att gaa aat atc	939
98	Lys Ile Ser Glu Arg Leu Val Ile Thr Ser Glu Met Ile Glu Asn Ile	
99	255 260 265	
101	caa tct gtt aag gca tac tgc tgg gaa gaa gca atg gaa aaa atg att	987
102	Gln Ser Val Lys Ala Tyr Cys Trp Glu Glu Ala Met Glu Lys Met Ile	
103	270 275 280 285	
105	gaa aac tta aga caa aca gaa ctg aaa ctg act cgg aag gca gcc tat	1035
106	Glu Asn Leu Arg Gln Thr Glu Leu Lys Leu Thr Arg Lys Ala Ala Tyr	
107	290 295 300	
109	gtg aga tac ttc aat agc tca gcc ttc ttc tca ggg ttc ttt gtg	1083
110	Val Arg Tyr Phe Asn Ser Ser Ala Phe Phe Phe Ser Gly Phe Phe Val	
111	305 310 315	
113	gtg ttt tta tct gtg ctt ccc tat gca cta atc aaa gga atc atc ctc	1131
114	Val Phe Leu Ser Val Leu Pro Tyr Ala Leu Ile Lys Gly Ile Ile Leu	
115	320 325 330	
117	cgg aaa ata ttc acc acc atc tca ttc tgc att gtt ctg cgc atg gcg	1179
118	Arg Lys Ile Phe Thr Thr Ile Ser Phe Cys Ile Val Leu Arg Met Ala	
119	335 340 345	
121	gtc act cgg caa ttt ccc tgg gct gta caa aca tgg tat gac tct ctt	1227
122	Val Thr Arg Gln Phe Pro Trp Ala Val Gln Thr Trp Tyr Asp Ser Leu	
123	350 355 360 365	
125	gga gca ata aac aaa ata cag gat ttc tta caa aag caa gaa tat aag	1275
126	Gly Ala Ile Asn Lys Ile Gln Asp Phe Leu Gln Lys Gln Glu Tyr Lys	
127	370 375 380	
129	aca ttg gaa tat aac tta acg act aca gaa gta gtg atg gag aat gta	1323
130	Thr Leu Glu Tyr Asn Leu Thr Thr Glu Val Val Met Glu Asn Val	
131	385 390 395	
133	aca gcc ttc tgg gag gag gga ttt ggg gaa tta ttt gag aaa gca aaa	1371

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134	Thr Ala Phe Trp Glu Glu Gly Phe Gly Glu Leu Phe Glu Lys Ala Lys			
135	400	405	410	
137	caa aac aat aac aat aga aaa act tct aat ggt gat gac agc ctc ttc	1419		
138	Gln Asn Asn Asn Asn Arg Lys Thr Ser Asn Gly Asp Asp Ser Leu Phe			
139	415	420	425	
141	ttc agt aat ttc tca ctt ctt ggt act cct gtc ctg aaa gat att aat	1467		
142	Phe Ser Asn Phe Ser Leu Leu Gly Thr Pro Val Leu Lys Asp Ile Asn			
143	430	435	440	445
145	ttc aag ata gaa aga gga cag ttg ttg gcg gtt gct gga tcc act gga	1515		
146	Phe Lys Ile Glu Arg Gly Gln Leu Leu Ala Val Ala Gly Ser Thr Gly			
147	450	455	460	
149	gca ggc aag act tca ctt cta atg atg att atg gga gaa ctg gag cct	1563		
150	Ala Gly Lys Thr Ser Leu Leu Met Met Ile Met Gly Glu Leu Glu Pro			
151	465	470	475	
153	tca gag ggt aaa att aag cac agt gga aga att tca ttc tgt tct cag	1611		
154	Ser Glu Gly Lys Ile Lys His Ser Gly Arg Ile Ser Phe Cys Ser Gln			
155	480	485	490	
157	ttt tcc tgg att atg cct ggc acc att aaa gaa aat atc atc ttt ggt	1659		
158	Phe Ser Trp Ile Met Pro Gly Thr Ile Lys Glu Asn Ile Ile Phe Gly			
159	495	500	505	
161	gtt tcc tat gat gaa tat aga tac aga agc gtc atc aaa gca tgc caa	1707		
162	Val Ser Tyr Asp Glu Tyr Arg Tyr Arg Ser Val Ile Lys Ala Cys Gln			
163	510	515	520	525
165	cta gaa gag gac atc tcc aag ttt gca gag aaa gac aat ata gtt ctt	1755		
166	Leu Glu Glu Asp Ile Ser Lys Phe Ala Glu Lys Asp Asn Ile Val Leu			
167	530	535	540	
169	gga gaa ggt gga atc aca ctg agt gga ggt caa cga gca aga att tct	1803		
170	Gly Glu Gly Gly Ile Thr Leu Ser Gly Gly Gln Arg Ala Arg Ile Ser			
171	545	550	555	
173	tta gca aga gca gta tac aaa gat gct gat ttg tat tta tta gac tct	1851		
174	Leu Ala Arg Ala Val Tyr Lys Asp Ala Asp Leu Tyr Leu Leu Asp Ser			
175	560	565	570	
177	cct ttt gga tac cta gat gtt tta aca gaa aaa gaa ata ttt gaa agc	1899		
178	Pro Phe Gly Tyr Leu Asp Val Leu Thr Glu Lys Glu Ile Phe Glu Ser			
179	575	580	585	
181	tgt gtc tgt aaa ctg atg gct aac aaa act agg att ttg gtc act tct	1947		
182	Cys Val Cys Lys Leu Met Ala Asn Lys Thr Arg Ile Leu Val Thr Ser			
183	590	595	600	605
185	aaa atg gaa cat tta aag aaa gct gac aaa ata tta att ttg aat gaa	1995		
186	Lys Met Glu His Leu Lys Lys Ala Asp Lys Ile Leu Ile Leu Asn Glu			
187	610	615	620	
189	ggt agc agc tat ttt tat ggg aca ttt tca gaa ctc caa aat cta cag	2043		
190	Gly Ser Ser Tyr Phe Tyr Gly Thr Phe Ser Glu Leu Gln Asn Leu Gln			
191	625	630	635	
193	cca gac ttt agc tca aaa ctc atg gga tgt gat tct ttc gac caa ttt	2091		
194	Pro Asp Phe Ser Ser Lys Leu Met Gly Cys Asp Ser Phe Asp Gln Phe			
195	640	645	650	
197	agt gca gaa aga aga aat tca atc cta act gag acc tta cac cgt ttc	2139		
198	Ser Ala Glu Arg Arg Asn Ser Ile Leu Thr Glu Thr Leu His Arg Phe			

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199	655	660	665	2187
201	tca tta gaa gga gat gct cct gtc tcc tgg aca gaa aca aaa aaa caa			
202	Ser Leu Glu Gly Asp Ala Pro Val Ser Trp Thr Glu Thr Lys Lys Gln		685	
203	670	675	680	2235
205	tct ttt aaa cag act gga gag ttt ggg gaa aaa agg aag aat tct att			
206	Ser Phe Lys Gln Thr Gly Glu Phe Gly Lys Arg Lys Asn Ser Ile		700	
207	690	695	700	2283
209	ctc aat cca atc aac tct ata cga aaa ttt tcc att gtg caa aag act			
210	Leu Asn Pro Ile Asn Ser Ile Arg Lys Phe Ser Ile Val Gln Lys Thr		715	
211	705	710	715	2331
213	ccc tta caa atg aat ggc atc gaa gag gat tct gat gag cct tta gag			
214	Pro Leu Gln Met Asn Gly Ile Glu Glu Asp Ser Asp Glu Pro Leu Glu		730	
215	720	725	730	2379
217	aga agg ctg tcc tta gta cca gat tct gag cag gga gag gcg ata ctg			
218	Arg Arg Leu Ser Leu Val Pro Asp Ser Glu Gln Gly Glu Ala Ile Leu		745	
219	735	740	745	2427
221	cct cgc atc agc gtg atc agc act ggc ccc acg ctt cag gca cga agg			
222	Pro Arg Ile Ser Val Ile Ser Thr Gly Pro Thr Leu Gln Ala Arg Arg		765	
223	750	755	760	2475
225	agg cag tct gtc ctg aac ctg atg aca cac tca gtt aac caa ggt cag			
226	Arg Gln Ser Val Leu Asn Leu Met Thr His Ser Val Asn Gln Gly Gln		780	
227	770	775	780	2523
229	aac att cac cga aag aca aca gca tcc aca cga aaa gtg tca ctg gcc			
230	Asn Ile His Arg Lys Thr Thr Ala Ser Thr Arg Lys Val Ser Leu Ala		795	
231	785	790	795	2571
233	cct cag gca aac ttg act gaa ctg gat ata tat tca aga agg tta tct			
234	Pro Gln Ala Asn Leu Thr Glu Leu Asp Ile Tyr Ser Arg Arg Leu Ser		810	
235	800	805	810	2619
237	caa gaa act ggc ttg gaa ata agt gaa gaa att aac gaa gac tta			
238	Gln Glu Thr Gly Leu Glu Ile Ser Glu Glu Ile Asn Glu Asp Leu		825	
239	815	820	825	2667
241	aag gag tgc ctt ttt gat gat atg gag agc ata cca gca gtg act aca			
242	Lys Glu Cys Leu Phe Asp Asp Met Glu Ser Ile Pro Ala Val Thr Thr		845	
243	830	835	840	2715
245	tgg aac aca tac ctt cga tat att act gtc cac aag agc tta att ttt			
246	Trp Asn Thr Tyr Leu Arg Tyr Ile Thr Val His Lys Ser Leu Ile Phe		860	
247	850	855	860	2763
249	gtg cta att tgg tgc tta gta att ttt ctg gca gag gtg gct gct tct			
250	Val Leu Ile Trp Cys Leu Val Ile Phe Leu Ala Glu Val Ala Ala Ser		875	
251	865	870	875	2811
253	ttg gtt gtg ctg tgg ctc ctt gga aac act cct ctt caa gac aaa ggg			
254	Leu Val Val Leu Trp Leu Leu Gly Asn Thr Pro Leu Gln Asp Lys Gly		890	
255	880	885	890	2859
257	aat agt act cat agt aga aat aac agc tat gca gtg att atc acc agc			
258	Asn Ser Thr His Ser Arg Asn Asn Ser Tyr Ala Val Ile Ile Thr Ser		905	
259	895	900	905	2907
261	acc agt tcg tat tat gtg ttt tac att tac gtg gga gta gcc gac act			
262	Thr Ser Ser Tyr Tyr Val Phe Tyr Ile Tyr Val Gly Val Ala Asp Thr		925	
263	910	915	920	

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265	ttg ctt gct atg gga ttc ttc aga ggt cta cca ctg gtg cat act cta	2955		
266	Leu Leu Ala Met Gly Phe Arg Gly Leu Pro Leu Val His Thr Leu			
267	930	940		
269	atc aca gtg tcg aaa att tta cac cac aaa atg tta cat tct gtt ctt	3003		
270	Ile Thr Val Ser Lys Ile Leu His His Lys Met Leu His Ser Val Leu			
271	945	955		
273	caa gca cct atg tca acc ctc aac acg ttg aaa gca ggt ggg att ctt	3051		
274	Gln Ala Pro Met Ser Thr Leu Asn Thr Leu Lys Ala Gly Gly Ile Leu			
275	960	970		
277	aat aga ttc tcc aaa gat ata gca att ttg gat gac ctt ctg cct ctt	3099		
278	Asn Arg Phe Ser Lys Asp Ile Ala Ile Leu Asp Asp Leu Leu Pro Leu			
279	975	985		
281	acc ata ttt gac ttc atc cag ttg tta att gtc att gga gct ata	3147		
282	Thr Ile Phe Asp Phe Ile Gln Leu Leu Leu Val Ile Gly Ala Ile			
283	990	1000	1005	
285	gca gtt gtc gca gtt tta caa ccc tac atc ttt gtt gca aca gtg cca	3195		
286	Ala Val Val Ala Val Leu Gln Pro Tyr Ile Phe Val Ala Thr Val Pro			
287	1010	1015	1020	
289	gtg ata gtg gct ttt att atg ttg aga gca tat ttc ctc caa acc tca	3243		
290	Val Ile Val Ala Phe Ile Met Leu Arg Ala Tyr Phe Leu Gln Thr Ser			
291	1025	1030	1035	
293	cag caa ctc aaa caa ctg gaa tct gaa ggc agg agt cca att ttc act	3291		
294	Gln Gln Leu Lys Gln Leu Glu Ser Glu Gly Arg Ser Pro Ile Phe Thr			
295	1040	1045	1050	
297	cat ctt gtt aca agc tta aaa gga cta tgg aca ctt cgt gcc ttc gga	3339		
298	His Leu Val Thr Ser Leu Lys Gly Leu Trp Thr Leu Arg Ala Phe Gly			
299	1055	1060	1065	
301	cgg cag cct tac ttt gaa act ctg ttc cac aaa gct ctg aat tta cat	3387		
302	Arg Gln Pro Tyr Phe Glu Thr Leu Phe His Lys Ala Leu Asn Leu His			
303	1070	1075	1080	1085
305	act gcc aac tgg ttc ttg tac ctg tca aca ctg cgc tgg ttc caa atg	3435		
306	Thr Ala Asn Trp Phe Leu Tyr Leu Ser Thr Leu Arg Trp Phe Gln Met			
307	1090	1095	1100	
309	aga ata gaa atg att ttt gtc atc ttc att gct gtt acc ttc att	3483		
310	Arg Ile Glu Met Ile Phe Val Ile Phe Phe Ile Ala Val Thr Phe Ile			
311	1105	1110	1115	
313	tcc att tta aca aca gga gaa gga aga gtt ggt att atc ctg	3531		
314	Ser Ile Leu Thr Gly Glu Gly Glu Gly Arg Val Gly Ile Ile Leu			
315	1120	1125	1130	
317	act tta gcc atg aat atc atg agt aca ttg cag tgg gct gta aac tcc	3579		
318	Thr Leu Ala Met Asn Ile Met Ser Thr Leu Gln Trp Ala Val Asn Ser			
319	1135	1140	1145	
321	agc ata gat gtg gat agc ttg atg cga tct gtg agc cga gtc ttt aag	3627		
322	Ser Ile Asp Val Asp Ser Leu Met Arg Ser Val Arg Val Phe Lys			
323	1150	1155	1160	1165
325	ttc att gag atg cca aca gaa ggt aaa cct acc aag tca acc aaa cca	3675		
326	Phe Ile Asp Met Pro Thr Glu Gly Lys Pro Thr Lys Ser Thr Lys Pro			
327	1170	1175	1180	
329	tac aag aat ggc caa ctc tcg aaa gtt atg att att gag aat tca cac	3723		

VERIFICATION SUMMARY
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